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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/799,910DATE: 11/26/97
TIME: 13:57:20

INPUT SET: S21738.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

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General Information

(i) APPLICANT: Falb, Dean

(ii) TITLE OF THE INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF
CARDIOVASCULAR DISEASE

(iii) NUMBER OF SEQUENCES: 44

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: PENNIE & EDMONDS LLP
(B) STREET: 1155 Avenue of the Americas
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10036-2711

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 2.0

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/799,910
(B) FILING DATE: 13-FEB-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 60/011,787
(B) FILING DATE: 16-FEB-1996

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Coruzzi, Laura A
(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7853-067-999

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212)7909090
(B) TELEFAX: (212)8699741
(C) TELEX: 66141 PENNIE

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(2) INFORMATION FOR SEQ ID NO:1:

50

51

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1953 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

56

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(ii) MOLECULE TYPE: cDNA

58

(ix) FEATURE:

59

60

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 162...1871
(D) OTHER INFORMATION:

63

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

66

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GGCACGAGTC GGAGCCGGGC GGAGGGGAGG GGGGAAAGAG GAGCGCAGGG TGAGAGTGAG 60
CCGCAGGCTT CGGGAGGCCA GGGGGCGGGG GGAGCAGCGC CGAGGYCGCC GCCTCCGCCT 120
CCGCCGCCTA GGACTAGGGG GTGGGGGACG GACAAGCCCC G ATG CCG GGG GAG ACG 176
Met Pro Gly Glu Thr

1

5

71

72

GAA GAG CCG AGA CCC CCG GAG CAG CAG GAC CAG GAA GGG GGA GAG GCG 224
Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln Glu Gly Gly Glu Ala
10 15 20

75

76

GCC AAG GCG GCT CCG GAG CCC CAA CAA CGG CCC CCT GAG GCG GTC 272
Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg Pro Pro Glu Ala Val
25 30 35

79

80

GCG GCG GCG CCT GCA GGG ACC ACT AGC AGC CGC GTG CTG AGG GGA GGT 320
Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg Val Leu Arg Gly Gly
40 45 50

83

CGG GAC CGA GGC CGG GCC GCT GCG GCC GCC GCC GCA GCT GTG TCC 368
Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala Ala Ala Ala Val Ser
55 60 65

88

CGC CGG AGG AAG GCC GAG TAT CCC CGC CGG CGG AGG AGC AGC CCC AGC 416
Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg Ser Ser Pro Ser
70 75 80 85

91

GCC AGG CCT CCC GAC GTC CCC GGG CAG CAG CCC CAG GCC GCG AAG TCC 464
Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro Gln Ala Ala Lys Ser
90 95 100

95

CCG TCT CCA GTT CAG GGC AAG AAG AGT CCG CGA CTC CTA TGC ATA GAA 512
Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg Leu Leu Cys Ile Glu
105 110 115

99

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100	AAA GTA ACA ACT GAT AAA GAT CCC AAG GAA GAA AAA GAG GAA GAA GAC	560
101	Lys Val Thr Thr Asp Lys Asp Pro Lys Glu Glu Lys Glu Glu Glu Asp	
102	120 125 130	
104		
105	GAT TCT GCC CTC CCT CAG GAA GTT TCC ATT GCT GCA TCT AGA CCT AGC	608
106	Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala Ala Ser Arg Pro Ser	
107	135 140 145	
108		
109	CGG GGC TGG CGT AGT AGT AGG ACA TCT GTT TCT CGC CAT CGT GAT ACA	656
110	Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser Arg His Arg Asp Thr	
111	150 155 160 165	
112		
113	GAG AAC ACC CGA AGC TCT CGG TCC AAG ACC GGT TCA TTG CAG CTC ATT	704
114	Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile	
115	170 175 180	
116		
117	TGC AAG TCA GAA CCA AAT ACA GAC CAA CTT GAT TAT GAT GTT GGA GAA	752
118	Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp Tyr Asp Val Gly Glu	
119	185 190 195	
120		
121	GAG CAT CAG TCT CCA GGT GGC ATT AGT GGT GAA GAG GAA GAG GAG GAG	800
122	Glu His Gln Ser Pro Gly Gly Ile Ser Gly Glu Glu Glu Glu Glu Glu	
123	200 205 210	
124		
125	GAA GAA GAG ATG TTA ATC AGT GAA GAG GAG ATA CCA TTC AAA GAT GAT	848
126	Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp	
127	215 220 225	
128		
129	CCA AGA GAT GAG ACC TAC AAA CCC CAC TTA GAA AGG GAA ACC CCA AAG	896
130	Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys	
131	230 235 240 245	
132		
133	CCA CGG AGA AAA TCA GGG AAG GTA AAA GAA GAG AAG GAG AAG AAG GAA	944
134	Pro Arg Arg Lys Ser Gly Lys Val Lys Glu Glu Lys Glu Lys Lys Glu	
135	250 255 260	
136		
137	ATT AAA GTG GAA GTA GAG GTG GAG GTG AAA GAA GAG GAG AAT GAA ATT	992
138	Ile Lys Val Glu Val Glu Val Glu Val Lys Glu Glu Glu Asn Glu Ile	
139	265 270 275	
140		
141	AGA GAG GAT GAG GAA CCT CCA AGG AAG AGA GGA AGA AGA CGA AAA GAT	1040
142	Arg Glu Asp Glu Glu Pro Pro Arg Lys Arg Gly Arg Arg Arg Lys Asp	
143	280 285 290	
144		
145	GAC AAA AGT CCA CGT TTA CCC AAA AGG AGA AAA AAG CCT CCA ATC CAG	1088
146	Asp Lys Ser Pro Arg Leu Pro Lys Arg Arg Lys Lys Pro Pro Ile Gln	
147	295 300 305	
148		
149	TAT GTC CGT TGT GAG ATG GAA GGA TGT GGA ACT GTC CTT GCC CAT CCT	1136
150	Tyr Val Arg Cys Glu Met Glu Gly Cys Gly Thr Val Leu Ala His Pro	
151	310 315 320 325	
152		

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153	CGC TAT TTG CAG CAC CAC ATT AAA TAC CAG CAT TTG CTG AAG AAG AAA	1184
154	Arg Tyr Leu Gln His His Ile Lys Tyr Gln His Leu Leu Lys Lys	
155	330	335
156		340
157	TAT GTA TGT CCC CAT CCC TCC TGT GGA CGA CTC TTC AGG CTT CAG AAG	1232
158	Tyr Val Cys Pro His Pro Ser Cys Gly Arg Leu Phe Arg Leu Gln Lys	
159	345	350
160		355
161	CAA CTT CTG CGA CAT GCC AAA CAT CAT ACA GAT CAA AGG GAT TAT ATC	1280
162	Gln Leu Leu Arg His Ala Lys His His Thr Asp Gln Arg Asp Tyr Ile	
163	360	365
164		370
165	TGT GAA TAT TGT GCT CGG GCC TTC AAG AGT TCC CAC AAT CTG GCA GTG	1328
166	Cys Glu Tyr Cys Ala Arg Ala Phe Lys Ser Ser His Asn Leu Ala Val	
167	375	380
168		385
169	CAC CGG ATG ATT CAC ACT GGC GAG AAG CCA TTA CAA TGT GAG ATC TGT	1376
170	His Arg Met Ile His Thr Gly Glu Lys Pro Leu Gln Cys Glu Ile Cys	
171	390	395
172		400
173	GGA TTT ACT TGT CGA CAA AAG GCA TCT CTT AAT TGG CAC ATG AAG AAA	1424
174	Gly Phe Thr Cys Arg Gln Lys Ala Ser Leu Asn Trp His Met Lys Lys	
175	410	415
176		420
177	CAT GAT GCA GAC TCC TTC TAC CAG TTT TCT TGC AAT ATC TGT GGC AAA	1472
178	His Asp Ala Asp Ser Phe Tyr Gln Phe Ser Cys Asn Ile Cys Gly Lys	
179	425	430
180		435
181	AAA TTT GAG AAG AAG GAC AGC GTA GTG GCA CAC AAG GCA AAA AGC CAC	1520
182	Lys Phe Glu Lys Lys Asp Ser Val Val Ala His Lys Ala Lys Ser His	
183	440	445
184		450
185	CCT GAG GTG CTG ATT GCA GAA GCT CTG GCT GCC AAT GCA GGC GCC CTC	1568
186	Pro Glu Val Leu Ile Ala Glu Ala Leu Ala Ala Asn Ala Gly Ala Leu	
187	455	460
188		465
189	ATC ACC AGC ACA GAT ATC TTG GGC ACT AAC CCA GAG TCC CTG ACG CAG	1616
190	Ile Thr Ser Thr Asp Ile Leu Gly Thr Asn Pro Glu Ser Leu Thr Gln	
191	470	475
192		480
193	485	
194	CCT TCA GAT GGT CAG GGT CTT CCT CTT CCT GAG CCC TTG GGA AAC	1664
195	Pro Ser Asp Gly Gln Gly Leu Pro Leu Leu Pro Glu Pro Leu Gly Asn	
196	490	495
197		500
198	TCA ACC TCT GGA GAG TGC CTA CTG TTA GAA GCT GAA GGG ATG TCA AAG	1712
199	Ser Thr Ser Gly Glu Cys Leu Leu Leu Glu Ala Glu Gly Met Ser Lys	
200	505	510
201		515
202	TCA TAC TGC AGT GGG ACG GAA CGG GTG AGC CTG ATG GCT GAT GGG AAG	1760
203	Ser Tyr Cys Ser Gly Thr Glu Arg Val Ser Leu Met Ala Asp Gly Lys	
204	520	525
205		530
	ATC TTT GTG GGA AGC GGC AGC AGT GGA GGC ACT GAA GGG CTG GTT ATG	1808

RAW SEQUENCE LISTING
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206 Ile Phe Val Gly Ser Gly Ser Ser Gly Gly Thr Glu Gly Leu Val Met
 207 535 540 545
 208
 209 AAC TCA GAT ATA CTC GGT GCT ACC ACA GAG GTT CTG ATT GAA GAT TCA 1856
 210 Asn Ser Asp Ile Leu Gly Ala Thr Thr Glu Val Leu Ile Glu Asp Ser
 211 550 555 560 565
 212
 213 GAC TCT GCC GGA CCT TAGTGGACAG GAAGACTTGG GGCATGGGAC AGCTCAGACT T 1912
 214 Asp Ser Ala Gly Pro
 215 570
 216
 217 TGTATTTAAA AGTTAAAAAG GACAAAAAAA AAAAAAAA A 1953
 218
 219 (2) INFORMATION FOR SEQ ID NO:2:
 220
 221 (i) SEQUENCE CHARACTERISTICS:
 222 (A) LENGTH: 570 amino acids
 223 (B) TYPE: amino acid
 224 (C) STRANDEDNESS: unknown
 225 (D) TOPOLOGY: unknown
 226
 227 (ii) MOLECULE TYPE: protein
 228 (v) FRAGMENT TYPE: internal
 229
 230 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
 231
 232 Met Pro Gly Glu Thr Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln
 233 1 5 10 15
 234 Glu Gly Gly Glu Ala Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg
 235 20 25 30
 236 Pro Pro Glu Ala Val Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg
 237 35 40 45
 238 Val Leu Arg Gly Gly Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala
 239 50 55 60
 240 Ala Ala Ala Val Ser Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg
 241 65 70 75 80
 242 Arg Ser Ser Pro Ser Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro
 243 85 90 95
 244 Gln Ala Ala Lys Ser Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg
 245 100 105 110
 246 Leu Leu Cys Ile Glu Lys Val Thr Thr Asp Lys Asp Pro Lys Glu Glu
 247 115 120 125
 248 Lys Glu Glu Glu Asp Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala
 249 130 135 140
 250 Ala Ser Arg Pro Ser Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser
 251 145 150 155 160
 252 Arg His Arg Asp Thr Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly
 253 165 170 175
 254 Ser Leu Gln Leu Ile Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp
 255 180 185 190
 256 Tyr Asp Val Gly Glu Glu His Gln Ser Pro Gly Gly Ile Ser Gly Glu
 257 195 200 205
 258 Glu Glu Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile

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SEQUENCE VERIFICATION REPORT
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Original Text